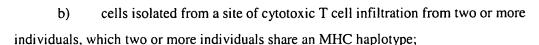
## WHAT IS CLAIMED IS:

- 1. A method for identifying a cytotoxic T cell epitope comprising the steps in order of:
- a) contacting a population of at least two cytotoxic T cells having the same MHC-haplotype restriction with
  - i) a library of molecules attached to solid phase supports by a releasable linker, wherein each solid phase support is attached to a single species of molecule, and wherein the structure of the molecule can be determined, which library of molecules contains a conserved structural motif corresponding to a structural motif characteristic of peptides that associate with the MHC-haplotype to which the cytotoxic T cells are restricted; and
  - ii) antigen presentation means, which antigen presentation means correspond to the MHC-haplotype to which the cytotoxic T cells are restricted;

wherein the solid phase supports of the library are in separate fractions;

- b) cleaving at least a portion of the releasable linker so as to release at least a portion of the molecule;
- c) evaluating whether the cytotoxic T cells recognize a molecule present in one or more of the fractions of the library of molecules;
- d) isolating one or more solid phase support(s) from the fractions; and
- e) determining the structure of a molecule on a solid phase support isolated from the fraction.
- 2. The method according to claim 1, wherein the cytotoxic T cells are selected from the group consisting of
- a) polyclonal T cells isolated from a site of cytotoxic T cell infiltration from an individual;



- c) two or more cytotoxic T cell lines; and
- d) any combination thereof.
- 3. The method according to claim 2, wherein the site of cytotoxic T cell infiltration is a tumor.
- 4. The method according to claim 1, wherein the molecules are peptides.
- 5. The method according to claim 4, wherein the peptides comprise subunits selected from the group consisting of glycine, L-amino acids, D-amino acids, non-classical amino acids, and peptidomimetics.
- 6. The method according to claim 1, wherein the solid phase support is selected from the group consisting of polystyrene resin, poly(dimethylacryl)amide-grafted styrene-co-divinylbenzene resin, polyamide resin, polystyrene resin grafted with polyethylene glycol, and polydimethylacrylamide resin.
- 7. The method according to claim 1, wherein the releasable linker releases upon exposure to an acid, a base, a nucleophile, an electrophile, light, an oxidizing agent, a reducing agent, or an enzyme.
- 8. The method according to claim\_L, wherein the structural motif contained in the library of molecules is selected from the group consisting of LXXXXXXV (SEQ ID NO: 1); RXXXXXXX + (SEQ ID NO: 2); X(D, E) XXXXXXX(F, K, Y) (SEQ ID NO: 3); RXXXXXXL (SEQ ID NO: 4); X(K, R)XXXXXX(L, I) (SEQ ID NO: 5); (M, L)XXXXXXK (SEQ ID NO: 6); EXXXXXXX(Y, F) (SEQ ID NO: 7); XPXXXXX(F, H, W, Y) (SEQ ID NO:8); (L, I)XXXXXX(H, K) (SEQ ID NO:9); wherein X indicates any amino acid residue, and + indicates a positively charged amino acid residue.
- 9. The method according to claim 4, wherein a limited number of representative amino acid residues are incorporated in the peptides of the library.

- 10. The method according to claim 9, wherein positively charged amino acid residues are substituted with an amino acid selected from the group consisting of lysine, arginine, and histidine; negatively charged amino acid residues are substituted with an amino acid selected from the group consisting of aspartic acid and glutamic acid; neutral, polar amino acid residues are substituted with an amino acid selected from the group consisting of asparagine, glutamine, serine, threonine, tyrosine, glycine and cysteine; nonpolar amino acid residues are substituted with an amino acid selected from the group consisting of alanine, valine, leucine, isoleucine, proline, phenylalanine, tryptophan, and methionine.
- 11. The method according to claim 10, wherein the nonpolar, aromatic amino acid residues are substituted with an amino acid selected from the group consisting of tyrosine, threonine, and tryptophan; and the nonpolar aliphatic amino acid residues are substituted with an amino acid selected from the group consisting of alanine, valine, leucine, isoleucine, proline, and methionine.
- 12. The method according to claim 1, further comprising a coding molecule attached to each solid phase support of the library, which coding molecule defines the structure of the molecule attached to the solid phase support by the releasable linker.
- 13. The method according to claim 12, wherein the coding molecule is selected from the group consisting of a peptide and an oligonucleotide.
- 14. The method according to claim 10, wherein the coding molecule is an inert molecular tag that can be decoded by gas-phase chromatography.
- 15. The method according to claim 1, wherein the antigen presentation means is selected from the group consisting of a purified MHC class I molecule complexed to  $\beta_2$ -microglobulin; an intact antigen presenting cell; and a foster antigen presenting cell.
- 16. The method according to claim 1, wherein the antigen presentation means is a foster antigen presenting cell.

- 17. The method according to claim 16, wherein the foster antigen presenting cell lacks antigen processing activity, whereby it expresses MHC molecules free of bound peptides.
- 18. The method according to claim 17, wherein the foster antigen presenting cell is cell line 174xCEM. T2.
- 19. The method according to claim 1, wherein the recognition of a molecule present in one or more of the fractions of the library of molecules by the cytotoxic T cells is evaluated by detecting cytotoxic T cell activation.
- 20. The method according to claim 19, wherein cytotoxic T cell activation is detected by a method selected from the group consisting of <sup>3</sup>H-thymidine incorporation; metabolic activity detected by conversion of MTT to formazan blue; increased cytokine mRNA expression; increased cytokine protein production; and chromium release by target cells.
- 21. The method of claim 1, wherein the structure of the molecule is determined by analyzing a portion of the molecule remaining on the solid phase support.
- 22. The method according to claim 4, wherein a sequence of the peptide is determined by sequencing a portion of the peptide remaining on the solid phase support.
- 23. The method according to claim 12, wherein the structure of the molecule is determined by analyzing the structure of the coding molecule.
- 24. The method according to claim 1, wherein the structure of the molecule is determined after isolating more than one candidate solid phase support; repeating steps a) through c), isolating one solid phase support in step c), and determining the structure of a molecule on the solid phase support isolated in step c).
- 25. The method according to claim 9, further comprising the steps in order of:
- a) contacting the population of at least two cytotoxic T cells having the same MHC-haplotype restriction with

- i) a library of molecules attached to solid phase supports by a releasable linker, wherein each solid phase support is attached to a single species of molecule, and wherein the structure of the molecule can be determined, which library of molecules contains a conserved structural motif corresponding to a structural motif characteristic of peptides that associate with the MHC-haplotype to which the cytotoxic T cells are restricted, and wherein every amino acid corresponding to the representative residue is utilized at the position identified for the corresponding representative residue; and
- ii) antigen presentation means, which antigen presentation means correspond to the MHC-haplotype to which the cytotoxic T cells are restricted;

wherein the solid phase supports of the library are in separate fractions;

- b) cleaving at least a portion of the releasable linker so as to release at least a portion of the molecule;
- c) evaluating whether the cytotoxic T cells recognize a molecule present in one or more of the fractions of the library of molecules;
- d) isolating one or more solid phase support(s) from the fractions; and
- e) determining the structure of a molecule on a solid phase support isolated from the fraction.
- 26. A method for identifying a high affinity cytotoxic T cell epitope comprising:
- a) contacting a population of cytotoxic T cells having an MHC-haplotype restriction with
  - i) a library of molecules attached to solid phase supports by a releasable linker, wherein each solid phase support is attached to a single species of molecule, and wherein the structure of the molecule can be determined, which library of molecules contains a conserved structural motif corresponding to a structural motif characteristic of peptides that associate with the MHC-haplotype to which the cytotoxic T cells are restricted, and wherein every amino acid corresponding to a representative residue determined according to the method of

claim 9 is utilized at the position identified for the corresponding representative residue; and

ii) antigen presentation means, which antigen presentation means correspond to the MHC-haplotype to which the cytotoxic T cells are restricted;

wherein the solid phase supports of the library are in separate fractions;

- b) cleaving at least a portion of the releasable linker so as to release at least a portion of the molecule;
- c) evaluating whether the cytotoxic T cells recognize a molecule present in one or more of the fractions of the library of molecules;
- d) isolating one or more solid phase support(s) from the fractions; and
- e) determining the structure of a molecule on a solid phase support isolated from the fraction.
- 27. A method of identifying a protein antigen comprising:
- a) identifying the cytotoxic T cell epitope of the protein according to the method of claim 25;
- b) comparing a sequence of the T cell epitope identified in step (a) with known sequences of proteins; and
- c) determining a protein having a sequence corresponding to the sequence of the T cell epitope.
- 28. A method of identifying a protein antigen comprising:
- a) identifying the cytotoxic T cell epitope of the protein according to the method of claim 26;
- b) comparing a sequence of the T cell epitope identified in step (a) with known sequences of proteins; and
- c) determining a protein having a sequence corresponding to the sequence of the T cell epitope.